

Genetic specificities of the acetylation system in patients with erysipelas

Kazan Federal University, 420008, Kremlevskaya 18, Kazan, Russia

Abstract

© 2018, Dynasty Publishing House. All rights reserved. The objective. To study a contribution of polymorphic variants of the N-acetyltransferase 2 detoxification system gene to the formation of predisposition to erysipelas infection and to establish associative relationships with the clinical course of disease. Patients and methods. The observation included 92 patients with erysipelas (basic group) aged 22 to 88 years (63.38 ± 11.85), of them 72.8% were women. The control group consisted of conditionally healthy individuals ($n = 71$), who did not have a history of the disease under study and were comparable with the basic group by gender (70.4% of women, 29.6% of men, $p > 0.05$) and age (58.34 ± 6.93 years; $p > 0.05$). The material for molecular-genetic examinations was peripheral blood. Genotyping was performed by the method of polymerase chain reaction. Results. Distribution of the NAT2 gene polymorphisms in the group of patients with erysipelas ($n = 92$) and in the control group of healthy individuals ($n = 71$) has shown the presence of the G/A NAT2 Gly286Glu genotype associations with the development of erysipelas. We have found associative relationships between the C/T NAT2 Leu161Leu and C/C NAT2 Leu161Leu genotypes and the character of local process. A risk for development of erysipelas in women is associated with the C/C NAT2 Leu161Leu genotype, in men with G/A NAT2 Gly286Glu. Conclusion. Polymorphisms in the NAT2 gene influence the predisposition to the development of erysipelas and specificities of the clinical course of disease.

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Keywords

Detoxification, Erysipelas, Genetic polymorphism, N-acetyltransferase

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